

In the Claims

1-56 (Canceled).

57 (Previously presented). An isolated polypeptide comprising:

- a) SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10;
- b) a fusion protein comprising SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10; or
- c) an active variant of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10, wherein any amino acid specified in the sequence is non-conservatively substituted, provided that no more than 15% of the amino acid residues are substituted and said active variant prevents the terminal differentiation of preadipocytes.

58 (Previously presented). The isolated polypeptide according to claim 57, wherein said isolated polypeptide comprises SEQ ID NO: 2 or SEQ ID NO: 3.

59 (Previously presented). The isolated polypeptide according to claim 57, wherein said isolated polypeptide comprises SEQ ID NO: 4.

60 (Previously presented). The isolated polypeptide according to claim 57, wherein said isolated polypeptide is a fusion protein comprising SEQ ID NO: 2 or SEQ ID NO: 3.

61 (Previously presented). The isolated polypeptide according to claim 57, wherein said isolated polypeptide is a fusion protein comprising SEQ ID NO: 4.

62 (Currently amended). The isolated polypeptide according to claim 60, wherein SEQ ID NO: 2 or SEQ ID NO: 3 is fused to one or more amino acid ~~sequence~~ sequences selected from: a membrane-bound protein, an immunoglobulin constant region, multimerization domains, extracellular proteins, signal peptide-containing proteins, or export signal-containing proteins.

63 (Previously presented). The isolated polypeptide according to claim 61, wherein SEQ ID NO: 4 is fused to one or more amino acid sequences selected from: a membrane-bound protein, an immunoglobulin constant region, multimerization domains, extracellular proteins, signal peptide-containing proteins, or export signal-containing proteins.

64 (Previously presented). The isolated polypeptide according to claim 57, wherein said isolated polypeptide is an active variant of SEQ ID NO: 2 or SEQ ID NO: 3, wherein any amino acid specified in the sequence is non-conservatively substituted, provided that no more than 15% of the amino acid residues are substituted and said active variant prevents the terminal differentiation of preadipocytes.

65 (Previously presented). The isolated polypeptide according to claim 57, wherein said isolated polypeptide is an active variant of SEQ ID NO: 4, wherein any amino acid specified in the sequence is non-conservatively substituted, provided that no more than 15% of the amino acid residues are substituted and said active variant prevents the terminal differentiation of preadipocytes.

66 (Previously presented). The isolated polypeptide according to claim 64, wherein no more than 10% of the amino acid residues are substituted.

67 (Previously presented). The isolated polypeptide according to claim 64, wherein no more than 5% of the amino acid residues are substituted.

68 (Previously presented). The isolated polypeptide according to claim 65, wherein no more than 10% of the amino acid residues are substituted.

69 (Previously presented). The isolated polypeptide according to claim 65, wherein no more than 5% of the amino acid residues are substituted.

70 (Previously presented). A method of making a polypeptide comprising transforming an isolated host cell with a polynucleotide encoding a polypeptide comprising:

- a) SEQ ID NO: 2 or SEQ ID NO:4;
- b) a fusion protein comprising SEQ ID NO: 2 or SEQ ID NO: 4; or
- c) an active variant of SEQ ID NO: 2 or SEQ ID NO: 4, wherein any amino acid specified in the sequence is non-conservatively substituted, provided that no more than 15% of the amino acid residues are substituted and said active variant prevents the terminal differentiation of preadipocytes;

and culturing said transformed host cell under conditions that allow for the expression of said polypeptide.

71 (Previously presented). The method according to claim 70, wherein said polypeptide comprises SEQ ID NO: 2 or SEQ ID NO: 3.

72 (Previously presented). The method according to claim 70, wherein said polypeptide comprises SEQ ID NO: 4.

73 (currently amended). The method according to claim 70, wherein said polypeptide is a fusion protein comprising SEQ ID NO: 2 ~~or~~ SEQ ID NO: 3.

74 (Previously presented). The method according to claim 70, wherein said polypeptide is a fusion protein comprising SEQ ID NO: 4.

75 (Previously presented). The method according to claim 73, wherein SEQ ID NO: 2 or SEQ ID NO: 3 is fused to one or more amino acid sequences selected from: a membrane-bound protein, an immunoglobulin constant region, multimerization domains, extracellular proteins, signal peptide-containing proteins, or export signal-containing proteins.

76 (Previously presented). The method according to claim 74, wherein SEQ ID NO: 4 is fused to one or more amino acid sequences selected from: a membrane-bound protein, an immunoglobulin constant region, multimerization domains, extracellular proteins, signal peptide-containing proteins, or export signal-containing proteins.

77 (Previously presented). The method according to claim 70, wherein said polypeptide is an active variant of SEQ ID NO: 2 or SEQ ID NO: 3, wherein any amino acid specified in the sequence is non-conservatively substituted, provided that no more than 15% of the amino acid residues are substituted and said active variant prevents the terminal differentiation of preadipocytes.

78 (Previously presented). The method according to claim 70, wherein said polypeptide is an active variant of SEQ ID NO: 4, wherein any amino acid specified in the sequence is non-conservatively substituted, provided that no more than 15% of the amino acid residues are substituted and said active variant prevents the terminal differentiation of preadipocytes.

79 (Previously presented). The method according to claim 77, wherein no more than 10% of the amino acid residues are substituted.

80 (Previously presented). The method according to claim 77, wherein no more than 5% of the amino acid residues are substituted.

81 (Previously presented). The method according to claim 78, wherein no more than 10% of the amino acid residues are substituted.

82 (Previously presented). The method according to claim 78, wherein no more than 5% of the amino acid residues are substituted.